

SEQUENCE LISTING

<110> Presnell, Scott R.
Kuestner, Rolf E.
Gao, Zeren

<120> Human Cytokine Receptor

<130> 00-49

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (86)...(2344)

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agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga	256
Arg Met Lys Ala Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly	
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Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys	
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Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser	
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Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu	
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Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg	
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Ser	Gly	Leu	Gly	Glu	Glu	Glu	Pro	Pro	Ala	Leu	Pro	Ser	Lys	Leu	Leu	
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<213> Homo sapiens

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 35 40 45
 Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn
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 Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr
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 Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
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 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
 100 105 110
 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
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 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
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 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
 145 150 155 160
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
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 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
 180 185 190
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
 195 200 205
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
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 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
 225 230 235 240

Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
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 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
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 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
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 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
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 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
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 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
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 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
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 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
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 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
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<212> DNA

<213> Artificial Sequence

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<222> (86)...(2344)

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Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys	
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Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile	
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Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln	
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Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe	
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ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga	496
Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg	
125 130 135	
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Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser	
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 Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp
 220 225 230

cac gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag 832
 His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys
 235 240 245

ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa 880
 Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln
 250 255 260 265

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 300 305 310

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 Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr
 315 320 325

ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca	1120
Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser	
330 335 340 345	
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His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu	
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Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu	
395 400 405	
gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag	1360
Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys	
410 415 420 425	
atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag	1408
Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys	
430 435 440	
tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc	1456
Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly	
445 450 455	
tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa	1504
Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu	
460 465 470	
aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt	1552
Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe	
475 480 485	
atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc	1600

1120
 1168
 1216
 1264
 1312
 1360
 1408
 1456
 1504
 1552
 1600

Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile	
490 495 500 505	
cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc	1648
Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu	
510 515 520	
tgt tcc cac ctg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag	1696
Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln	
525 530 535	
cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc	1744
His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly	
540 545 550	
cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag	1792
Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu	
555 560 565	
gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca	1840
Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro	
570 575 580 585	
ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tgc ggc ttg gtt	1888
Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val	
590 595 600	
tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta	1936
Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu	
605 610 615	
aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag	1984
Lys Val Glu Ala Ala Val Leu Glu Ala Thr Gly Pro Ala Asp Ser Gln	
620 625 630	
cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct	2032
His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro	
635 640 645	
gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa	2080
Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys	
650 655 660 665	

gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat gac tcg 2128
 Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser
 670 675 680

tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg 2176
 Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser
 685 690 695

acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct 2224
 Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser
 700 705 710

tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc 2272
 Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu
 715 720 725

tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat 2320
 Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp
 730 735 740 745

gaa ctc cac gcg gcc gcc cct ttg taacaaaacg aaagagtcta agcattgcc 2374
 Glu Leu His Ala Ala Ala Pro Leu
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ctttagctg 2383

<210> 5

<211> 753

<212> PRT

<213> Homo sapiens

<400> 5

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 Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg
 35 40 45
 Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn
 50 55 60
 Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr
 65 70 75 80

Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
 85 90 95
 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
 100 105 110
 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
 115 120 125
 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
 130 135 140
 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
 145 150 155 160
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
 165 170 175
 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
 180 185 190
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
 195 200 205
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
 210 215 220
 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
 225 230 235 240
 Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
 245 250 255
 Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser Cys
 260 265 270
 Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp
 275 280 285
 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
 290 295 300
 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
 305 310 315 320
 Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg
 325 330 335
 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
 340 345 350
 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro
 355 360 365
 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
 370 375 380
 Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly
 385 390 395 400
 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu
 405 410 415

Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
 420 425 430
 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
 435 440 445
 Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe
 450 455 460
 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
 465 470 475 480
 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
 485 490 495
 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
 500 505 510
 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
 515 520 525
 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
 530 535 540
 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
 545 550 555 560
 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
 565 570 575
 Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val
 580 585 590
 Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys
 595 600 605
 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu
 610 615 620
 Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly
 625 630 635 640
 Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala
 645 650 655
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
 660 665 670
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
 675 680 685
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser
 690 695 700
 Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Glu
 705 710 715 720
 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala
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 Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Ala Ala Pro
 740 745 750

Leu

<210> 6
 <211> 2259
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> This degenerate nucleotide sequence encodes the
 amino acid sequence of SEQ ID NO:5.

<221> misc_feature
 <222> (1)..(2259)
 <223> n = A,T,C or G

<400> 6

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tggmgnatga	argcngcngc	nmgnccnmgn	ytntgygtng	cnaaygargg	ngtnggnccn	180
gcwnsmgna	aywsnggnyt	ntayaayath	acnttyaart	aygayaaytg	yacnacntay	240
ytnaayccng	tnggnaarca	ygtcnathgcn	gaygcncara	ayathacnat	hwsncartay	300
gcntgycayg	aycargtngc	ngtnacnath	ytntggwsnc	cngnggcnyt	nggnathgar	360
ttyytnaarg	gnttymngnt	nathytngar	garytnaarw	sngarggnmg	ncartgygar	420
carytnathy	tnaargaycc	naarcarytn	aaywsnwsnt	tyaarmgnac	nggnatggar	480
wsncarcnt	ttyttnaayat	gaarttygar	acngaytayt	tygtnaargt	ngtncntty	540
ccwnsnatha	araaygarws	naaytaycay	ccnttytyt	tymgnacnmg	ngcntgygay	600
ytnytnytn	arccngayaa	yytngcntgy	aarccnttyt	ggaarccnmg	naayytnaay	660
athwsncarc	ayggnwsnga	yatgcargtn	wsnttygayc	aygcncncna	yaaytytggn	720
ttymgnttyt	tytattytnca	ytayaarytn	aarcaygarg	gncnttyaa	rmgnaaracn	780
tgyaarcarg	arcaracnac	ngaratgacn	wsntgyytny	tncaraaygt	nwsnccnggn	840
gaytayatha	thgarytngt	ngaygayacn	aayacnacnm	gnaargtnat	gcaytaygcn	900
ytnaarccng	tncaysncc	ntgggcnggn	ccnathmgng	cngtngcnat	hacngtncn	960
ytngtngtna	thwsngcntt	ygcnacnytn	ttyacngtna	tgtgymgnaa	raarcarcar	1020
garaayatht	aywsncayyt	ngaygargar	wsnwsngarw	snwsnacnta	yacngcngcn	1080
ytncnmgng	armgnytnmg	nccnmgnccn	aargtnttyy	tntgtyayws	nwsnaargay	1140
ggncaraayc	ayatgaaygt	ngtncartgy	ttygcntayt	ttytncarga	yttytggygn	1200
tggygargtng	cnytngayyt	ntgggargay	tywsnytn	gymngargg	ncarmnggar	1260
tgggtnathc	araarathca	ygarwsncar	tyathathg	tngtntgyws	naarggnatg	1320
aartayttyg	tngayaaara	raaytayaar	cayaarggng	gngngmgngg	nwsnggnaar	1380
ggngarytnt	tyytngtngc	ngtnwsngcn	athgcngara	arytnmgna	rgcnaarcar	1440
wsnwsnwsng	cngcnytnws	naarttyath	gcngtntayt	tygaytayws	ntgygarggn	1500
gaygtncngc	gnathytnga	yytnwsnacn	aartaymgny	tnatggayaa	yytnccncar	1560
ytntgywsnc	ayytncayws	nmngngaycay	ggnytncarg	arccngngna	rcayacnmgn	1620

carggnwsnm gnmgnaayta yttymgnwsn aarwsnggnm gnwsnynta ygtngcnath	1680
tgyaayatgc aycarttyat hgaygargar ccngaytgg tygaraarca rttygtncn	1740
ttycayccnc cncnnytnmg ntaymgngar ccngtnyng araarttyga ywsnggnytn	1800
gtnytnaayg aygtnatgtg yaarcnngn ccngarwsng aytytgyt naargtngar	1860
gcngcngtny tngngcnac nggncnngn gaywsncarc aygarwsnca rcayggnggn	1920
ytngaycarg ayggngargc nmgnccnngn ytngaygnw sngcngcnyt ncarccnytn	1980
ytncaacng tnaargcngg nwsnccnwsn gayatgccnm gngaywsngg nathtaygay	2040
wsnwsngtn cwnswnsga rytwnsnytn ccnytnatgg arggnytnws nacngaycar	2100
acngaracnw snwsnytnac ngarwsngtn wsnwsnwnw snggnytnng ngargargar	2160
ccncngcny tncnwnsnaa rytnytnwsn wsnngnwsnt gyaargcnga yytnngntgy	2220
mgnwsntaya cngaygaryt ncaygcngcn gcncnytn	2259

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<211> 2341

<212> DNA

<213> Homo sapiens

<220>

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Met Ala Pro Trp Leu Gln Leu Cys Ser	
1 5	

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg	160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val	
10 15 20 25	

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg	208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp	
30 35 40	

agg gga gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc	256
Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr	
45 50 55	

ttc aaa tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat	304
Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His	
60 65 70	

gtg att gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His 75 80 85	352
gac caa gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile 90 95 100 105	400
gaa ttc ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu 110 115 120	448
gga aga cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn 125 130 135	496
agt agc ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met 140 145 150	544
aaa ttt gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile 155 160 165	592
aaa aac gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys 170 175 180 185	640
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cct cgg aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser 205 210 215	736
ttc gac cat gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His 220 225 230	784
tac aag ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln 235 240 245	832

gag caa act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca	880
Glu Gln Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro	
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ggg gat tat ata att gag ctg gtg gat gac act aac aca aca aga aaa	928
Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys	
270 275 280	
gtg atg cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc	976
Val Met His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro	
285 290 295	
atc aga gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc	1024
Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe	
300 305 310	
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Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile	
315 320 325	
tat tca cat tta gat gaa gag agc tct gag tct tcc aca tac act gca	1120
Tyr Ser His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala	
330 335 340 345	
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Ala Leu Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys	
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Tyr Ser Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe	
365 370 375	
gcc tac ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg	1264
Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu	
380 385 390	
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Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile	
395 400 405	
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Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly	
410 415 420 425	
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Met Lys Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly	
430 435 440	
cga ggc tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att	1456
Arg Gly Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile	
445 450 455	
gcc gaa aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc	1504
Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser	
460 465 470	
aag ttt atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc	1552
Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro	
475 480 485	
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Gly Ile Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro	
490 495 500 505	
cag ctc tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg	1648
Gln Leu Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro	
510 515 520	
ggg cag cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag	1696
Gly Gln His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys	
525 530 535	
tca ggc cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att	1744
Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile	
540 545 550	
gac gag gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct	1792
Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro	
555 560 565	
cct cca ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc	1840
Pro Pro Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly	
570 575 580 585	

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cgg cct gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg Arg Pro Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr 635 640 645	2032
gtg aaa gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat Val Lys Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr 650 655 660 665	2080
gac tcg tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly 670 675 680	2128
ctc tcg acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc Leu Ser Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser 685 690 695	2176
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ctc ctc tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac Leu Leu Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr 715 720 725	2272
act gat gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta Thr Asp Glu Leu His Ala Val Ala Pro Leu 730 735	2322
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<210> 8
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 8

Met	Ala	Pro	Trp	Leu	Gln	Leu	Cys	Ser	Val	Phe	Phe	Thr	Val	Asn	Ala
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		20						25					30		
Ala	Arg	Gly	Ala	Asp	Thr	Cys	Gly	Trp	Arg	Gly	Val	Gly	Pro	Ala	Ser
	35						40					45			
Arg	Asn	Ser	Gly	Leu	Tyr	Asn	Ile	Thr	Phe	Lys	Tyr	Asp	Asn	Cys	Thr
	50					55					60				
Thr	Tyr	Leu	Asn	Pro	Val	Gly	Lys	His	Val	Ile	Ala	Asp	Ala	Gln	Asn
65				70					75					80	
Ile	Thr	Ile	Ser	Gln	Tyr	Ala	Cys	His	Asp	Gln	Val	Ala	Val	Thr	Ile
			85					90						95	
Leu	Trp	Ser	Pro	Gly	Ala	Leu	Gly	Ile	Glu	Phe	Leu	Lys	Gly	Phe	Arg
			100					105					110		
Val	Ile	Leu	Glu	Glu	Leu	Lys	Ser	Glu	Gly	Arg	Gln	Cys	Gln	Gln	Leu
		115					120					125			
Ile	Leu	Lys	Asp	Pro	Lys	Gln	Leu	Asn	Ser	Ser	Phe	Lys	Arg	Thr	Gly
	130					135					140				
Met	Glu	Ser	Gln	Pro	Phe	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	Tyr	Phe
145					150					155				160	
Val	Lys	Val	Val	Pro	Phe	Pro	Ser	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	His
			165					170						175	
Pro	Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro	Asp
			180					185					190		
Asn	Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	Ser
		195					200				205				
Gln	His	Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His	Asn
	210					215					220				
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 Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
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 Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
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 Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
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 Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
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 Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
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 Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
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 Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu
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 Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
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 Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
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 Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
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 Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
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 Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
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<213> Artificial Sequence

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<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:8.

<221> misc_feature

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<223> n = A,T,C or G

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athacnathw sncartaygc ntgcaygay cargtngcng tncnathyt ntggwsnccn	300
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gtnaargtn tncnttycc nwsnathaar aaygarwsna aytaycaycc nttyttyty	540
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aarccnmgna ayytnaayat hwsncarcay ggnwsngaya tgcargtnws nttygaycay	660
gcncncaya ayytygntt ymgnttytyt tayytncayt ayaarytnaa rcaygarggn	720
ccttyaarm gnaaracntg yaarcargar caracnacng aracnacnws ntgyytnytn	780

caraaygtnw	sncnngnga	ytayathath	garytngtng	aygayacnaa	yacnacnmgn	840
aargtnatgc	aytaycny	naarccngtn	caywsnccnt	ggcngngncc	nathmngcn	900
gtngcnatha	cngtncnyt	ngtngtnath	wsngcnytyg	cnacnytnnt	yacngtnatg	960
tgymgnaara	arcarcarga	raayathtay	wsncayytng	aygargarws	nwsngarwsn	1020
wsnacntaya	cngcngcny	nccnmngar	mgnytnmgnc	cnmgncnaa	rgtnttytn	1080
tgytaywsnw	snaargaygg	ncaraaycay	atgaaygtng	tncartgytt	ygcntaytty	1140
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ttytgyytna	argtngargc	ngcngtnytn	ggngcnacng	gnccngcnga	ywsncarcay	1860
garwsncarc	ayggnggny	ngaycargay	ggngargcnm	gnccngcny	ngayggnwsn	1920
gcngcnytn	arcnnytny	ncayacngtn	aargcnggnw	sncnwsnga	yatgcnmgn	1980
gaywsnggna	thtaygayws	nwsngtnccn	wsnwsngary	tnwsnytncc	nytnatggar	2040
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<212> PRT

<213> Artificial Sequence

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<223> Peptide linker.

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Met Ala Pro Trp Leu	
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cag ctc tgc tcc ttc ttc ttc act gtc aac gcc tgt ctc aac ggc tcg	163
Gln Leu Cys Ser Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser	
10 15 20	
cag ctg gca gtg gcc gcg ggc ggc tcc ggc cgc gcg agg ggc gcg gac	211
Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp	
25 30 35	
acc tgt ggc tgg agg gga gtg ggg ccg gcc agc agg aac agc gga ctg	259
Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu	
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His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro	
55 60 65	
ggc ggc ggg aag cat gcg att gct gat gct cag aac atc acc atc agc	355
Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser	
70 75 80 85	
cag tac gct tgc cac gac cag gtg gca gtc acc att ctt tgg tcc cca	403
Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro	
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Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu	
105 110 115	
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Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp	
120 125 130	
ccc aaa cag ctc aac agc agc ttc aga agg act gga atg gaa tct cag	547

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Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys Ile Val	
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cct ttc cct tcc att aaa aat gaa agc aat tac cat ccc ttc ttc ttc	643
Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe	
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aga aca cgg gcc tgt gac ctg ttg tta caa cct gac aac ttg gcc tgt	691
Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys	
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aag cct ttc tgg aag cct cga aac ctg aat atc agc cag cat ggt tct	739
Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser	
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Asp Met His Val Ser Phe Asp His Ala Pro Gln Asn Phe Gly Phe Arg	
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Gly Phe His Val Leu Tyr Lys Leu Lys His Glu Gly Pro Phe Arg Arg	
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Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr Thr Ser Cys Leu Leu	
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Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Ser	
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Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val Lys Ser Val Gln Ser	
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Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val	
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Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys	
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Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Pro Glu Ser	
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Ser Thr Tyr Ala Ala Leu Pro Arg Asp Arg Leu Arg Pro Gln Pro	
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Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly Gln Asn His Met Asn	
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Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu	
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Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln	
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Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val	
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Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn Phe Arg	
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His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly Glu Phe Leu Val	
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Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser	
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Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys	
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Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser Thr Lys Tyr Lys Leu	
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Met Asp His Leu Pro Glu Leu Cys Ala His Leu His Ser Gly Glu Gln	
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Glu Val Leu Gly Gln His Pro Gly His Ser Ser Arg Arg Asn Tyr Phe	
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Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His	
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Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Ile Pro	
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Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro Val Leu Glu Lys Phe	
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Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser Lys Pro Glu Pro Glu	
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Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val Leu Gly Ala Ala Gly	
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Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln His Val Gly Leu Asp	
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Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser Ala Pro Ala Leu Gln	
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Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro Ser Glu Met Pro Arg	
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Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu	
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Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile Glu Thr Ser Ser Leu	
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Thr Tyr Leu Asn Pro Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln
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 Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe
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 Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr
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 Phe Val Lys Ile Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr
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 His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro
 180 185 190
 Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile
 195 200 205
 Ser Gln His Gly Ser Asp Met His Val Ser Phe Asp His Ala Pro Gln
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 Asn Phe Gly Phe Arg Gly Phe His Val Leu Tyr Lys Leu Lys His Glu
 225 230 235 240
 Gly Pro Phe Arg Arg Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr
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 Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu
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 Leu Val Asp Asp Ser Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val
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 Lys Ser Val Gln Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile
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 Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val
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 325 330 335
 Glu Ser Pro Glu Ser Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg
 340 345 350
 Leu Arg Pro Gln Pro Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly
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 Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp
 370 375 380
 Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu
 385 390 395 400

Cys Arg Glu Gly Gln Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser
 405 410 415
 Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp
 420 425 430
 Lys Lys Asn Phe Arg His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly
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 Glu Phe Phe Leu Val Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln
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 Ala Lys Gln Ser Ser Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr
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 Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser
 485 490 495
 Thr Lys Tyr Lys Leu Met Asp His Leu Pro Glu Leu Cys Ala His Leu
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 His Ser Gly Glu Gln Glu Val Leu Gly Gln His Pro Gly His Ser Ser
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 Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
 530 535 540
 Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
 545 550 555 560
 Lys Gln Phe Ile Pro Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro
 565 570 575
 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser
 580 585 590
 Lys Pro Gly Pro Glu Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val
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 Leu Gly Ala Ala Gly Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln
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 His Val Gly Leu Asp Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser
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 Ala Pro Ala Leu Gln Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro
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 Ser Glu Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser
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Ala Pro Leu

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<213> Artificial Sequence

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<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:12.

<221> misc_feature

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gayaaytgya	cnacntayyt	naayccnggn	ggnggnaarc	aygcncathgc	ngaygcncar	240
aayathacna	thwsncarta	ycgntgyca	gaycargtng	cngtnacnat	hytntggwsn	300
ccnggngcny	tnggnathga	rttyytnaar	ggnttymgng	tnathytnga	rgarytnaar	360
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ttymgngmna	cnggnatgga	rwsncarcen	ttyytnaaya	tgaarttyga	racngaytay	480
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tggaarccnm	gnaayytnaa	yathwsncar	cayggnwsng	ayatgcaygt	nwsnttygay	660
caygcncnc	araaytytgg	nttymgnggn	ttycaygtny	tnayaaryt	naarcaygar	720
gngcncntty	gngmgngnac	ntgymgncar	gaycaraaya	cngaracnac	nwsntgyytn	780
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